RAW SEQUENCE LISTING
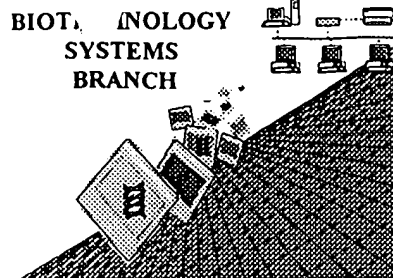# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/855, 886*

Source: *OiPE*

Date Processed by STIC: *5-29-01*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/855, 886 |

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
____Wrapped Aminos ·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
____   prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
____Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
____   ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
____   each n or Xaa can only represent a single residue. Please present the maximum number of each
____   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
____"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
____   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
____   the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
____   Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
____(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
____   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
____   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
____   This sequence is intentionally skipped .

____   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
____(NEW RULES)   <210> sequence id number
____   <400> sequence id number
____   000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
____(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
____   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ✓__Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
____Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
____   is Artificial Sequence

11 ✓·Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
____   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
____   "Unknown." Please explain source of genetic material in <220> to <223> section.
____   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
____"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
____   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

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        RAW SEQUENCE LISTING            DATE: 05/29/2001
        PATENT APPLICATION:  US/09/855,886     TIME: 11:17:57

        Input Set : A:\seqlist.txt
        Output Set: C:\CRF3\05292001\I855886.raw

   4 <110> APPLICANT: Coller et al.
   6 <120> TITLE OF INVENTION: METHOD OF INHIBITING ANGIOGENESIS AND
   7        TUMOR GROWTH AND PREVENTING TUMOR GROWTH AND METASTASES
  10 <130> FILE REFERENCE: A31386 070165.0489
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/855,886
  13 <141> CURRENT FILING DATE: 2001-05-15
  15 <150> PRIOR APPLICATION NUMBER: 09/090,757
  16 <151> PRIOR FILING DATE: 1998-06-04
  18 <160> NUMBER OF SEQ ID NOS: 2
  20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 13
  24 <212> TYPE: PRT
  25 <213> ORGANISM: Homo Sapiens
  28 <400> SEQUENCE: 1
  29  Cys Asn Gly Arg Cys Val Ser Gly Cys Ala Gly Arg Cys
  30    1          5                   10
  32 <210> SEQ ID NO: 2
  33 <211> LENGTH: 5
  34 <212> TYPE: PRT
  35 <213> ORGANISM: Synthetic
  37 <220> FEATURE:
W--> 38 <221> NAME/KEY: CYCLIC PEPTIDE
  39 <222> LOCATION: (0)...(0)
  40 <223> OTHER INFORMATION: (<200-203>) Xaa = D-Phenylalanine
  42 <400> SEQUENCE: 2
W--> 43  Arg Gly Asp Xaa Val
  44    1          5
  51 NY02:324961.1
```

Does Not Comply
Corrected Diskette Needed

Valid <213> responses are:
— Genus species of organism
— Unknown
— Artificial sequence

See #10 on the Error Summary Sheet. See also underlined portion of #11.

Delete extraneous material at the end of the file.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/855,886

DATE: 05/29/2001
TIME: 11:17:58

Input Set : **A:\seqlist.txt**
Output Set: **C:\CRF3\05292001\I855886.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:38 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2